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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2010; month=7; day=27; hr=11; min=15; sec=3; ms=141;]

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Reviewer Comments:

<400> 13

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His

1 5 10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
35 40 45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
50 55 60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
65 70 75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
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80 85 90

Please remove the blank line between the above row of codons and their respective amino acids; the amino acids should appear directly below their their codons.

<210> 15
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunk-2 gene revertant form, modified to be
heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1578)
<223> k = g or t.

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
1 5 10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147

Ser	Ile	Gly	Gly	Arg	Lys	Gln	Glu	Lys	Ala	Leu	Arg	Asn	Arg	Cys	Phe	
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Gly	Gly	Arg	Val	Ala	Ala	Thr	Thr	Gln	Cys	Ile	Leu	Thr	Ser	Asp	Ala	
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Cys	Pro	Glu	Thr	Leu	His	Ser	Gln	Thr	Gln	Ser	Ser	Arg	Lys	Asn	Tyr	
		65					70					75				
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Ala	Asp	Ala	Asn	Arg	Val	Ser	Ala	Ile	Ile	Leu	Gly	Gly	Gly	Thr	Gly	
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Phe	Ala	Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu	
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225				230				235																
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Pro	Val	Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp									
240				245				250																
cat	act	gga	cgt	gta	ctt	caa	ttc	ttt	gaa	aaa	cca	aag	ggg	gct	gat	819								
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415 420 425 430	
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Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val	
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495 500 505 510	
aac gat ggg tct gtc ata tagatcggct gcgctktgcg	1576
Asn Asp Gly Ser Val Ile	
515	

1) Please remove the blank line between the above row of codons and their amino acids; 2) the above <220>-<223> section describing "k" at

location 1578 is incorrect; the sequence only has 1576 nucleotides.
Same errors in Sequences 17, 19, 21, 23, 25, 27, 29, 31, 35, 37, 39 and 41.

<210> 33
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunk-2 gene revertant form, modified to be
heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1578)
<223> k = g or t.

<400> 33
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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
1 5 10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu

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				35				40				45					
ggt	ggt	aga	gtt	gct	gca	act	aca	caa	tgt	att	ctt	acc	tca	gat	gct	195	
Gly	Gly	Arg	Val	Ala	Ala	Thr	Thr	Gln	Cys	Ile	Leu	Thr	Ser	Asp	Ala		
				50				55				60					
tgt	cct	gaa	act	ctt	cat	tct	caa	aca	cag	tcc	tct	agg	aaa	aat	tat	243	
Cys	Pro	Glu	Thr	Leu	His	Ser	Gln	Thr	Gln	Ser	Ser	Arg	Lys	Asn	Tyr		
				65				70				75					
gct	gat	gca	aac	cgt	gta	tct	gck	atc	att	ttg	ggc	gga	ggc	act	gga	291	
Ala	Asp	Ala	Asn	Arg	Val	Ser	Ala	Ile	Ile	Leu	Gly	Gly	Gly	Thr	Gly		
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Ser	Gln	Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	Pro	Ala	Val	Pro		
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gtt	gga	gga	tgt	tac	agg	ctt	att	gat	atc	cct	atg	agt	aac	tgc	ttc	387	
Val	Gly	Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	Cys	Phe		
				115				120				125					
aac	agt	ggt	ata	aat	aag	ata	ttt	gtg	atg	agt	cag	ttc	aat	tct	act	435	
Asn	Ser	Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr		
				130				135				140					
tcg	ctt	aac	cgc	cat	att	cat	cgt	aca	tac	ctt	gaa	ggc	ggg	atc	aac	483	
Ser	Leu	Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn		
				145				150				155					
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Phe	Ala	Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu		
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gag	cca	gct	gga	tgg	ttc	cag	ggt	aca	gca	gac	tct	atc	aga	aaa	ttt	579	
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Val	Ile	Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu	
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cct	gtt	gat	gag	agc	cga	gct	tct	aaa	aat	ggg	cta	gtg	aag	att	gat	771
Pro	Val	Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp	
		240						245						250		
cat	act	gga	cgt	gta	ctt	caa	ttc	ttt	gaa	aaa	cca	aag	ggg	gct	gat	819
His	Thr	Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp	
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ttg	aat	tct	atg	aga	gtt	gag	acc	aac	ttc	ctg	agc	tat	gct	ata	gat	867
Leu	Asn	Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp	
						275									285	
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Asp	Ala	Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe	
			290												300	
aag	aaa	gat	gca	ctt	tta	gac	ctt	ctc	aag	tca	aaa	tat	act	caa	tta	963
Lys	Lys	Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu	
		305													315	
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His	Asp	Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	Met	Ser	
		320													330	
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370	375	380	
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc	1203		
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile			
385	390	395	
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Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile			
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gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg	1299		
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415	420	425	430
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta	1347		
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu			
435	440	445	
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Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly			
480	485	490	
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Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile			
495	500	505	510
aac gat ggg tct gtc ata tagatcggct gcgktktgcg	1576		
Asn Asp Gly Ser Val Ile			
515			

Two errors above: 1) the <220>-<223> section describing the "y" at location 1008 is errored: "g" is at locadtion 1008; 2) the <220>-<223> section describing the "k" at location 1578 is errored: there are only 1576 nucleotides above.

Application No: 10569000 Version No: 2.0

Input Set:

Output Set:

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Started:      2010-07-22 16:44:17.022
Finished:    2010-07-22 16:44:19.919
Elapsed:     0 hr(s) 0 min(s) 2 sec(s) 897 ms
Total Warnings: 0
Total Errors: 112
No. of SeqIDs Defined: 42
Actual SeqID Count: 42

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[illegible]

Input Set:

Output Set:

Started: 2010-07-22 16:44:17.022
Finished: 2010-07-22 16:44:19.919
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 897 ms
Total Warnings: 0
Total Errors: 112
No. of SeqIDs Defined: 42
Actual SeqID Count: 42

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> University of Florida Research Foundation, Inc.
Hannah, L. Curtis
Lyerly Linebarger, Carla R.

<120> Heat Stable Variants of Adenosine Diphosphate Glucose Pyrophosphorylase

<130> UF-371XC1 PCT

<140> 10569000

<141> 2010-07-22

<150> US 60/496,188

<151> 2003-08-18

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<212> PRT
<213> zea mays

<400> 2

Met	Asp	Met	Ala	Leu	Ala	Ser	Lys	Ala	Ser	Pro	Pro	Pro	Trp	Asn	Ala	1	5	10	15
Thr	Ala	Ala	Glu	Gln	Pro	Ile	Pro	Lys	Arg	Asp	Lys	Ala	Ala	Ala	Asn	20	25	30	
Asp	Ser	Thr	Tyr	Leu	Asn	Pro	Gln	Ala	His	Asp	Ser	Val	Leu	Gly	Ile	35	40	45	
Ile	Leu	Gly	Gly	Gly	Ala	Gly	Thr	Arg	Leu	Tyr	Pro	Leu	Thr	Lys	Lys	50	55	60	
Arg	Ala	Lys	Pro	Ala	Val	Pro	Leu	Gly	Ala	Asn	Tyr	Arg	Leu	Ile	Asp	65	70	75	80
Ile	Pro	Val	Ser	Asn	Cys	Leu	Asn	Ser	Asn	Ile	Ser	Lys	Ile	Tyr	Val	85	90	95	
Leu	Thr	Gln	Phe	Asn	Ser	Ala	Ser	Leu	Asn	Arg	His	Leu	Ser	Arg	Ala	100	105	110	
Tyr	Gly	Ser	Asn	Ile	Gly	Gly	Tyr	Lys	Asn	Glu	Gly	Phe	Val	Glu	Val	115	120	125	
Leu	Ala	Ala	Gln	Gln	Ser	Pro	Asp	Asn	Pro	Asn	Trp	Phe	Gln	Gly	Thr	130	135	140	
Ala	Asp	Ala	Val	Arg	Gln	Tyr	Leu	Trp	Leu	Phe	Glu	Glu	His	Asn	Val	145	150	155	160
Met	Glu	Phe	Leu	Ile	Leu	Ala	Gly	Asp	His	Leu	Tyr	Arg	Met	Asp	Tyr	165	170	175	

Glu	Lys	Phe	Ile	Gln	Ala	His	Arg	Glu	Thr	Asn	Ala	Asp	Ile	Thr	Val	180	185	190
Ala	Ala	Leu	Pro	Met	Asp	Glu	Lys	Arg	Ala	Thr	Ala	Phe	Gly	Leu	Met	195	200	205
Lys	Ile	Asp	Glu	Glu	Gly	Arg	Ile	Ile	Glu	Phe	Ala	Glu	Lys	Pro	Lys	210	215	220
Gly	Glu	Gln	Leu	Lys	Ala	Met	Met	Val	Asp	Thr	Thr	Ile	Leu	Gly	Leu	225	230	235
Asp	Asp	Val	Arg	Ala	Lys	Glu	Met	Pro	Tyr	Ile	Ala	Ser	Met	Gly	Ile	245	250	255
Tyr	Val	Phe	Ser	Lys	Asp	Val	Met	Leu	Gln	Leu	Leu	Arg	Glu	Gln	Phe	260	265	270
Pro	Glu	Ala	Asn	Asp	Phe	Gly	Ser	Glu	Val	Ile	Pro	Gly	Ala	Thr	Ser	275	280	285
Ile	Gly	Lys	Arg	Val	Gln	Ala	Tyr	Leu	Tyr	Asp	Gly	Tyr	Trp	Glu	Asp	290	295	300
Ile	Gly	Thr	Ile	Ala	Ala	Phe	Tyr	Asn	Ala	Asn	Leu	Gly	Ile	Thr	Lys	305	310	315
Lys	Pro	Ile	Pro	Asp	Phe	Ser	Phe	Tyr	Asp	Arg	Phe	Ala	Pro	Ile	Tyr	325	330	335
Thr	Gln	Pro	Arg	His	Leu	Pro	Pro	Ser	Lys	Val	Leu	Asp	Ala	Asp	Val	340	345	350
Thr	Asp	Ser	Val	Ile	Gly	Glu	Gly	Cys	Val	Ile	Lys	Asn	Cys	Lys	Ile	355	360	365
Asn	His	Ser	Val	Val	Gly	Leu	Arg	Ser	Cys	Ile	Ser	Glu	Gly	Ala	Ile	370	375	380
Ile	Glu	Asp	Ser	Leu	Leu	Met	Gly	Ala	Asp	Tyr	Tyr	Glu	Thr	Glu	Ala	385	390	395
Asp	Lys	Lys	Leu	Leu	Ala	Glu	Lys	Gly	Gly	Ile	Pro	Ile	Gly	Ile	Gly	405	410	415
Lys	Asn	Ser	Cys	Ile	Arg	Arg	Ala	Ile	Ile	Asp	Lys	Asn	Ala	Arg	Ile	420	425	430
Gly	Asp	Asn	Val	Lys	Ile	Leu	Asn	Ala	Asp	Asn	Val	Gln	Glu	Ala	Ala	435	440	445
Met	Glu	Thr	Asp	Gly	Tyr	Phe	Ile	Lys	Gly	Gly	Ile	Val	Thr	Val	Ile	450	455	460
Lys	Asp	Ala	Leu	Leu	Pro	Ser	Gly	Thr	Val	Ile						465	470	475

<210> 3
 <211> 1425
 <212> DNA
 <213> zea mays

<400> 3
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 cagccaattc caaagcgtga caaagccgct gcaaatgatt caacatgyct caatcctcaa 120
 gctcatgata gtgttcttgg aatcattctg ggaggtgggtg ctgggactag attgtacccc 180
 ttgacaaaga agcgtgccaa gcctgcagtg ccattgggtg ccaactatag actgattgat 240
 attcctgtca gcaattgtct caacagcaac atatccaaga tctatgtgct aacgcaatth 300
 aactctgctt ccctcaaccg tcacctctca agagcctacg ggagcaacat tggagggtac 360
 aagaatgaag ggtttgttga agtcttagct gcacagcaga gccagataa tccaaactgg 420
 tttcagggta ctgcagatgc tgtaaggcag tacttgtggt tgtttgagga gcataatgtg 480
 atggaatttc taattcttgc tggcgatcac ctgtaccgga tggactatga aaagttcatt 540
 caggcacaca gagaacaaaa tgctgatatt accgttgctg ccctaccgat ggatgagaaa 600
 cgtgcaactg catttggcct catgaaaatt gatgaagaag ggaggatcat tgagtttgct 660
 gagaaaccga aaggagagca gttgaaagca atgatggttg acaccaccat acttggcctt 720
 gatgacgtga gggcaaagga aatgccttat attgctagca tgggtatcta tgttttcagc 780
 aaagatgtaa tgcttcagct cctccgtgaa caatttctctg aagccaatga ctttggaagt 840
 gaggttattc caggtgcaac cagcattgga aagagggttc aggcttatct gtatgatggt 900
 tactgggaag atacgggtac cattgcgga ttttataatg caaacttggg aataaccaag 960
 aagccaatac cagatttcag cttctatgac cgttttgctc caatttatac acaacctcga 1020
 cacctgccac cttcaaaggt tcttgatgct gatgtgacag acagtgttat tggatgaagga 1080
 tgtgttatta aaaactgcaa gataaacat tctgtagttg gactccgatc ttgcatatct 1140
 gaaggtgcta tcatagagga cagtttacta atgggtgctg actactatga gacagaagct 1200
 gataaaaaac tccttgccga aaaagggtggc attcctattg gtattgggaa aaattcatgc 1260
 atcaggagag caatcattga caagaatgct cgaattggag acaatgttaa gatactcaat 1320
 gctgacaatg ttcaagaagc tgcaatggag acagacgggt acttcatcaa aggtggaatt 1380
 gtcacagtga tcaaggatgc ttactcct agtggacag ttata 1425

<210> 4
<211> 475

<212> PRT
<213> zea mays

<400> 4

Met Asp Met Ala Leu Ala Ser Lys Ala Ser Pro Pro Pro Trp Asn Ala
1 5 10 15

Thr Ala Ala Glu Gln Pro Ile Pro Lys Arg Asp Lys Ala Ala Ala Asn
20 25 30

Asp Ser Thr Cys Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly Ile
35 40 45

Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys
50 55 60

Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp
65 70 75 80

Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val
85 90 95

Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala
100 105 110

Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val
115 120 125

Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr
130 135 140

Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val
145 150 155 160

Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr
165 170 175

Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val
180 185 190

Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met
195 200 205

Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys
210 215 220

Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly Leu
225 230 235 240

Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile
245 250 255

Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln Phe
260 265 270

Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr Ser
275 280 285

Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu Asp
290 295 300

Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr Lys
305 310 315 320

Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile Tyr
325 330 335

Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp Val
340 345 350

Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys Ile
355 360 365

Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala Ile
370 375 380

Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu Ala
385 390 395 400

Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile Gly
405 410 415

Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg Ile
420 425 430

Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala Ala
435 440 445

Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val Ile
450 455 460

Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile
465 470 475

<210> 5
<211> 1428
<212> DNA
<213> zea mays

<400> 5
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cagccaattc caaagcgtga caaagccgct gcaaattgatt caacarcata cctcaatcct 120
caagctcatg atagtgttct tggaatcatt ctgggagggtg gtgctgggac tagattgtac 180
cccttgacaa agaagcgtgc caagcctgca gtgccattgg gtgccaaacta tagactgatt 240

gatattcctg tcagcaattg tctcaacagc aacatatcca agatctatgt gctaacgcaa 300
ttaactctg cttccctcaa ccgtcacctc tcaagagcct acgggagcaa cattggaggg 360
tacaagaatg aagggtttgt tgaagtctta gctgcacagc agagcccaga taatccaaac 420
tggtttcagg gtactgcaga tgctgtaagg cagtacttgt ggttgtttga ggagcataat 480
gtgatggaat ttctaattct tgctggcgat cacctgtacc ggatggacta tgaaaagttc 540
attcaggcac acagagaaac aaatgctgat attaccgttg ctgccctacc gatggatgag 600

aaacgtgcaa ctgcatttgg cctcatgaaa attgatgaag aaggaggat cattgagttt 660
gctgagaaaac cgaaaggaga gcagttgaaa gcaatgatgg ttgacaccac catacttggc 720
cttgatgacg tgagggcaaa ggaaatgcct tatattgcta gcatgggtat ctatgttttc 780
agcaaagatg taatgcttca gctcctccgt gaacaatttc ctgaagccaa tgactttgga 840
agtgaggtta ttccagggtc aaccagcatt ggaaagaggg ttcaggctta tctgtatgat 900
ggttactggg aagatatcgg taccattgcg gcattttata atgcaaactt gggaataacc 960
aagaagccaa taccagattt cagcttctat gaccgttttg ctccaattta tacacaacct 1020
cgacacctgc caccttcaaa ggttcttgat gctgatgtga cagacagtgt tattggtgaa 1080
ggatgtgtta ttaaaaactg caagataaac cattctgtag ttggactccg atcttgcata 1140
tctgaagggtg ctatcataga ggacagttta ctaatgggtg cggactacta tgagacagaa 1200
gctgataaaa aactccttgc cgaaaaaggt ggcatctcta ttggtattgg gaaaaattca 1260
tgcacagga gagcaatcat tgacaagaat gctcgaattg gagacaatgt taagatactc 1320
aatgctgaca atgttcaaga agctgcaatg gagacagacg ggtacttcat caaagggtga 1380
attgtcacag tgatcaagga tgctttactc cctagtggaa cagttata 1428

<210> 6

<211> 476

<212> PRT

<213> zea mays

<400> 6

Met Asp Met Ala Leu Ala Ser Lys Ala Ser Pro Pro Pro Trp Asn Ala
1 5 10 15

Thr Ala Ala Glu Gln Pro Ile Pro Lys Arg Asp Lys Ala Ala Ala Asn
20 25 30

Asp Ser Gln Thr Tyr Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly

35		40		45
Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys				
50		55		60
Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile				
65		70		80
Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr				
	85		90	95
Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg				
	100		105	110
Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu				
	115		120	125
Val Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly				
	130		135	140
Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn				
145		150		160
Val Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp				
	165		170	175
Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr				
	180		185	190
Val Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu				
	195		200	205
Met Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro				
	210		215	220
Lys Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly				
225		230		240
Leu Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly				
	245		250	255
Ile Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln				
	260		265	270
Phe Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr				
	275		280	285
Ser Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu				
	290		295	300
Asp Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr				
305		310		320
Lys Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile				
	325		330	335
Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp				

340		345		350
Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys				
355		360		365
Ile Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala				
370		375		380
Ile Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu				
385		390		395
				400
Ala Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile				
	405		410	415
Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg				
420				